

Date: November 20, 2001

Page 1

**TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US)  
CONCERNING A FILING UNDER 35 USC 371**

International Application No.: PCT/KR00/00535  
International Filing Date: May 25, 2000  
Priority Date Claimed: May 26, 1999  
Title of Invention: A METHOD FOR IDENTIFYING DNA MUTATION USING MICROWELL  
AND KIT THEREFOR  
Applicant(s) for DO/EO/US: Seung-Yong Hwang; Jin-Wook Jung; Cheol-Min Kim

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. (x) This is a **FIRST** submission of items concerning a filing under 35 USC 371.
2. () This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 USC 371.
3. (x) This express request to begin national examination procedures (35 USC 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 USC 371(b) and PCT Articles 22 and 39(1).
4. (x) A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. (x) A copy of the International Application as filed (35 USC 371(c)(2))
  - a) () is transmitted herewith (required only if not transmitted by the International Bureau).
  - b) (x) has been transmitted by the International Bureau.
  - c) (x) a copy of Form PCT/1B/308 is enclosed.
  - d) () is not required, as the application was filed in the United States Receiving Office (RO/US).
6. () A translation of the International Application into English (35 USC 371(c)(2)).
7. (x) Amendments to the claims of the International Application under PCT Article 19 (35 USC 371(c)(3))
  - a) () are transmitted herewith (required only if not transmitted by the International Bureau).
  - b) () have been transmitted by the International Bureau.
  - c) () have not been made; however, the time limit for making such amendments has NOT expired.
  - d) (x) have not been made and will not be made.
8. () A translation of the amendments to the claims under PCT Article 19 (35 USC 371(c)(3)).
9. (x) An oath or declaration of the inventor(s) (35 USC 371(c)(4)).
10. (x) A copy of the International Preliminary Examination Report with any annexes thereto, such as any amendments made under PCT Article 34.

Date: November 20, 2001

Page 2

11. ☐ A translation of the annexes, such as any amendments made under PCT Article 34, to the International Preliminary Examination Report under PCT Article 36 (35 USC 371(c)(5)).
12. ☒ An Information Disclosure Statement and PTO Form 1449 with 22 references (included) under 37 CFR 1.97 and 1.98.
13. ☒ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
14. ☒ A FIRST preliminary amendment.  
☐ A SECOND or SUBSEQUENT preliminary amendment.
15. ☐ A substitute specification.
16. ☐ A power of attorney and/or address letter.
17. ☒ International Application as published.
18. ☒ The present application qualifies for small entity status under 37 C.F.R. § 1.27.
19. ☒ A return prepaid postcard.
20. ☒ The following fees are submitted:

				FEES
<b>BASIC FEE</b>				\$1,040
<b>CLAIMS</b>	<b>NUMBER FILED</b>	<b>NUMBER EXTRA</b>	<b>RATE</b>	
Total Claims	18 - 20 =	0 ×	\$18	\$0
Independent Claims	2 - 3 =	0 ×	\$84	\$0
Multiple dependent claims(s) (if applicable)			\$280	\$0
<b>TOTAL OF ABOVE CALCULATIONS</b>				\$1,040
Reduction by 1/2 for filing by small entity (if applicable). Verified Small Entity statement must also be filed. (NOTE 37 CFR 1.9, 1.27, 1.28)				\$520
<b>TOTAL NATIONAL FEE</b>				\$520
<b>TOTAL FEES ENCLOSED</b>				\$520
amount to be refunded:				\$
amount to be charged:				\$

21. ☒ A check in the amount of \$520 to cover the above fees is enclosed.
22. ☒ Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40 per property.

U.S. Application No.  
Unknown

International Application No.  
PCT/KR00/00535

Attorney Docket No.  
HYLEE61.001APC

Date: November 20, 2001

Page 3

23. (x) The following forms are provided herewith:
- |                  |                  |
|------------------|------------------|
| (x) PCT/RO/101   | (x) PCT/ISA/210  |
| (x) PCT/IB/301   | (x) PCT/IB/304   |
| (x) PCT/IB/332   | (x) PCT/IPEA/402 |
| (x) PCT/IPEA/416 |                  |
24. (x) Paper copy of sequence listing; computer readable diskette containing sequence listing.
25. (x) The Commissioner is hereby authorized to charge only those additional fees which may be required, now or in the future, to avoid abandonment of the application, or credit any overpayment to Deposit Account No. 11-1410.

**NOTE:** Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

Che S. Chereskin  
Che Swyden Chereskin, Ph.D.  
Reg. No. 41,466  
Customer No. 20,995

H:\DOCS\CSC\CSC-2672.DOC  
112001

HYLEE61.001APC

PATENT

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant	:	Hwang, et al.	)	Group Art Unit : Unk
			)	
Appl. No.	:	Unknown	)	
			)	
Filed	:	Herewith	)	
			)	
For	:	A METHOD FOR IDENTIFYING	)	
		DNA MUTATION USING	)	
		MICROWELL AND KIT THEREFOR	)	
			)	
Examiner	:	Unknown	)	

---

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents  
Washington, D.C. 20231

Dear Sir:

Preliminary to examination on the merits, please amend the above-captioned U.S. application as follows:

IN THE SPECIFICATION

On page 1 of the Specification, after the Title of the Invention and before the Background of the Invention statement starting on line 1, please insert ---This is the U.S. National Phase under 35 U.S.C. § 371 of International Application PCT/KR00/00535, filed May 25, 2000, which claims priority of Korean Patent Application No. 10-1999-0019121, filed May 26, 1999.--

REMARKS

The specification has been amended to recite the International Application and priority application.

Appl. No. : Unknown  
Filed : Herewith

**Sequence listing**

A sequence listing and disk are submitted herewith. As required under 37 C.F.R. § 1.821 (f), I hereby verify that the data on the enclosed disk and the paper copies of the Sequence Listing are identical.

**Conclusion**

Should there be any questions concerning this application, the Examiner is invited to contact the undersigned agent at the telephone number appearing below.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: Nov. 20, 2001

By: Che S. Chereskin  
Che Swyden Chereskin, Ph.D.  
Registration No. 41,466  
Agent of Record  
620 Newport Center Drive  
Sixteenth Floor  
Newport Beach, CA 92660  
(949) 760-0404

H:\DOCS\CSC\CSC-2660.DOC  
111901

Rec'd PCT/PTO 20 NOV 2001

A METHOD FOR IDENTIFYING DNA MUTATION USING  
MICROWELLS AND KIT THEREFOR

5     BACKGROUND OF THE INVENTION

Field of the Invention

10       The present invention relates to a method for  
identifying DNA mutation using microwells and a kit  
therefor, more particularly, to an economical, simple and  
safe method for identifying single base mutations including  
substitution, insertion and deletion using microwells, and  
a kit therefor.

15       Background of the Invention

20       Techniques for determining the species of organisms  
and diagnosing diseases by identification of genes have  
been widely used in the art(see: J. Clin. Microbiol.,  
34:130-133, 1996). Diseases can be treated by using a  
variety of medications depending upon species and types of  
diseases. However, in such cases where the diseases are  
attributable to the infection with microorganisms which can  
25       be mutated, the use of conventional medication is limited.

30       Conventional techniques for detection of small  
mutations such as substitution, insertion and deletion in a  
DNA sequence includes dot blotting, RFLP(restriction  
fragment-length polymorphism) analysis, SSCP(single strand  
conformation polymorphism) analysis and DNA sequencing:

35       First, dot blotting technique employs the principle  
of Southern blotting, in which even a single base pair  
mismatch causes disruption of a DNA duplex above a certain  
temperature. This dot blotting can determine the presence  
of mutations through detection of signals created by a  
target sequence-represented oligonucleotide probe which has  
been prelabeled with a radioisotope, a fluorescent dye or

an enzyme connected to a chromogenic response when the oligonucleotide probe hybridizes nucleic acids immobilized on the membrane(see: British J. Dermatol., 131:72-77, 1994). Also, through the immobilization of an oligonucleotide probe on the membrane and preamplification of a target DNA, a mutation can be determined by the duplex formation between the immobilized oligonucleotide and the amplified DNA.

Secondly, RFLP analysis employs the characteristic of restriction enzymes which cleave only specific sequences. In other words, a normal nucleotide sequence amplified by PCR can be cleaved with a restriction enzyme while the corresponding nucleotide sequence with mutations on the recognition site cannot be cleaved by the same enzyme. After treating normal and mutated DNA samples with a restriction enzyme, the resulting mixtures of DNA fragments are subject to electrophoresis side by side on the same gel, and the presence of mutation can be determined by comparing the number of DNA fragments from each sample(see: Mol. Cell Biol., 279-281, 1995).

Thirdly, SSCP analysis employs the characteristic of single-stranded DNA in which its conformational changes caused by even a single point mutation give rise to changes in migration of the fragments in a non-denaturing gel. When the pattern of the restriction cleavage of a normal DNA and that of a mutant DNA remain the same, it is sometimes possible to detect changes in sequence by their effects on the migration of short fragments of single-stranded DNA, in a technique called SSCP. By comparing the migration patterns of mutated and non-mutated DNA strand in the non-denaturing gel, the presence or absence of mutation can be determined(see: Mol. Cell Biol., 289, 1995).

In addition to several techniques mentioned above, mutations can be detected by direct DNA sequencing through gel electrophoresis or using instruments(see: Mol. Cell Biol., 245-248, 1995). The said techniques which typically involve the use of radioactive material, fluorescent dye or enzyme for detection of signals, have

drawbacks such as safety problems and requiring high cost in waste disposal in case of radioactive labeling, and if not radioactive labeling, cumbersome and time consuming manipulation due to the use of membranes or performing an acrylamide gel electrophoresis.

Meanwhile, a microwell plate which has been used for identifying a protein with an antibody or identifying a specific nucleotide sequence by hybridizing with DNA or oligonucleotide can be used for determining the presence or absence of a mutation by employing the method of identifying a specific nucleotide sequence. For instance, a sample DNA is affixed to the microwell, and then identified with an oligonucleotide probe corresponding to the normal DNA sequence to be identified: i.e., a sample DNA amplified by PCR technique is affixed to a microwell, hybridizes with a biotin-bound probe, followed by the assessment of hybridization using an enzyme(see: Mol. Cell Probes, 6(1):79-85, 1992). The prior art method is, however, proven to be less satisfactory in the senses that it takes much time to analyze a sample DNA since the sample DNA has to be affixed to the microwell after collecting from a patient; due to the length of DNA, a sample DNA amplified by PCR may have a secondary structure which cause inhibition of hybridization with a probe; long-length DNA molecule may prevent its binding to the well(see: Anal. Biochem., 138-142, 1991); and, since a sample DNA is affixed to a microwell after denaturation into single strands, renaturation of the single-stranded DNA takes place easily during the period of experiment, which lowers the binding ability of sample DNA to the probe.

#### Summary of the Invention

In accordance with the present invention, it has been discovered that the mutations of DNA sequence can be identified in an economical, simple and safe manner by using microwells and a degradation enzyme which can bind to



biotin.

A primary object of the present invention is, therefore, to provide a method for identifying mutations in a DNA sequence whose corresponding normal sequence has already been determined, by amplifying target(sample) DNA through PCR and using microwells.

The other object of the invention is to provide a kit therefor with convenience.

#### BRIEF DESCRIPTION OF THE DRAWINGS

The above and the other objects and features of the present invention will become apparent from the following descriptions given in conjunction with the accompanying drawing, in which:

Figure 1 is a graph showing the results of identification of DNA mutations employing the method of the invention.

#### DETAILED DESCRIPTION OF THE INVENTION

The method for identifying DNA mutation using microwells comprises the steps of: preparing amplified biotinylated DNA fragments of a portion of nucleotide sequence to be identified by PCR using a biotin-bound primer; preparing a probe comprising normal sequence corresponding to the DNA sequence to be identified; affixing the probe thus prepared to the amine group of microwell; adding biotinylated DNA fragments thus prepared to the probe-affixed microwell; adding a streptavidin-linked degradation enzyme to the microwell in order to bind the degradation enzyme to biotin moiety of the probe; and, adding a substrate to be reacted with the degradation enzyme and detecting the color or absorbance change caused by degradation of the substrate.

Also, a kit for identifying DNA mutation comprises a microwell whose inside has amine group, 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide(EDC) solution and 1-methylimidazole solution, pH 7.0 for affixing a probe, 0.4M NaOH/0.25% Tween-20 solution for removing unaffixed probe, a solution containing dH<sub>2</sub>O, 20xSSPE/0.0167% Triton X-100 and salmon sperm DNA(10mg/ml) for blocking microwell surface, a solution of 0.5xSSC/0.1% Tween-20 for removing unhybridized biotinylated sample DNA fragments, a streptavidin-linked degradation enzyme to be bound to biotin, 100mM Tris-HCl(pH 7.5) solution containing 150mM NaCl for binding of streptavidin to biotin, 100mM Tris-HCl(pH 7.5) solution containing 150mM NaCl/0.1% Tween-20 for removing unbound streptavidin, and a substrate for the streptavidin-linked degradation enzyme.

In describing the specification, the term of 'mutation' is employed to mean a sequence variation such as substitution in which one or more nucleotides are substituted with another nucleotide(s), deletion in which one or more of existing nucleotides are deleted, and insertion in which one or more of additional nucleotides are inserted.

Mutations caused by one or more nucleotide changes frequently occur in microorganisms. For example, Mycobacterium tuberculosis which has a nucleotide change at a specific position is known to be resistant to rifampicin(see: Lancet 341:647-650, 1993). Therefore, detection of the presence or absence of mutations, moreover, identification of changed nucleotide sequences may be very useful in treatment of patients.

In accordance with the present invention, the method for identifying DNA mutation can be applied to detect not only the presence of mutations but also identify the types of mutations such as nucleotide substitution, insertion and deletion with ease. The method involves the following steps of preparing amplified sample DNA, preparing a probe,

affixing the probe to a microwell and detection of mutation by binding of sample DNA to the probe.

Step 1: Amplification of sample DNA

A portion of DNA sequence to be identified for mutation is amplified by polymerase chain reaction(PCR) employing a biotin-bound primer to give amplified biotinylated DNA fragments of sample: Since the PCR is carried out by employing a biotin-bound primer, the amplified product by PCR is a mixture of biotinylated and non-biotinylated nucleotide sequences which are complementary to each other.

Step 2: Preparation of probes

DNA probes which comprise normal sequences corresponding to the DNA sequences to be identified are prepared: The probes thus prepared consist of more than 10 nucleotides and contains a phosphate moiety at 5'end which enables the probe to be affixed to the amine group of microwell.

Step 3: Affixture of probes

The probes thus prepared are affixed to amine group on the inner surface of microwell: Since nucleotide sequences of synthesized probe may be reannealed spontaneously, the single stranded probes can be maintained by heating the probes for 5 to 15 minutes, most preferably for 10 minutes, at 90 to 100°C, most preferably at 94°C, followed by immediate cooling in ice water. Ice cold solutions of 10mM 1-methylimidazole, pH 7.0 and 10 mM 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide(EDC), pH 7.0 which catalyze the covalent-binding reaction of phosphate moiety of oligonucleotide and amine group on microwell are added to the single-stranded DNA probe. The probe

containing mixture was added to the amine-derivatized microwell, and the microwells are sealed with tape to prevent evaporation of reaction mixture, followed by incubation for 5 to 9 hours, most preferably for 7 hours, at 40 to 60°C, most preferably at 50°C. In this way, the probes are covalently affixed on the inner surface of microwell. Probe-affixed microwells are washed with 0.4M NaOH/0.25% Tween-20, and then with distilled water at room temperature.

Step 4: Addition of sample to the microwell

Biotinylated PCR fragments obtained in the previous step are added to the probe-affixed microwells: First, a solution containing dH<sub>2</sub>O, 20XSSPE/0.0167% Triton X-100 and salmon sperm DNA(10mg/ml) is added to microwells, and incubated for 10 to 20 minutes, most preferably for 15 minutes, at 40 to 60°C, most preferably at 50°C, to prevent biotinylated sample from binding to free amine group on the microwell surface. In order to denature biotinylated double-stranded DNA fragments obtained in Step 1 to allow hybridization with the probe, they are heated for 5 to 15 minutes, most preferably for 10 minutes, at 90 to 98°C, most preferably at 94°C, and chilled immediately in ice water. And then, a solution containing dH<sub>2</sub>O, 20XSSPE/0.0167% Triton X-100 and salmon sperm DNA (10mg/ml) is added to the single-stranded DNA sample. The mixture is introduced into the microwells, incubated for 5 to 15 hours, most preferably for 10 hours, at 50 to 70°C, most preferably at 60°C. After incubation, the residual mixture is removed, and microwells are washed with 0.5xSSC, 0.1% Tween-20. The sample with changed nucleotide sequence(s) would show low affinity for the probe affixed to microwell while the sample with normal sequence would show high affinity. Accordingly, biotin of the sample DNA fragments can be captured to the microwell, and the affinity difference between mutated and non-mutated sequences for

the probe can be measured in terms of the difference in density of microwell-bound biotin.

Step 5: Addition of a degradation enzyme

Streptavidin-linked degradation enzyme is added to the microwell in order to bind the degradation enzyme to biotin moiety of the probe-captured sample DNA fragment: To detect the difference in biotin density bound to the microwell of mutated and non-mutated DNA samples, degradation enzyme is bound to biotin. The degradation enzyme hydrolyzes a chromogenic substrate, and resulting changes in color intensity or absorbance can be measured. For example, streptavidin-alkaline phosphatase can be used; microwells are washed with a buffer solution of 100mM Tris-HCl(pH 7.5) containing 150mM NaCl/0.1% Tween-20, and streptavidin-alkaline phosphatase diluted with a buffer solution of 100mM Tris-HCl(pH 7.5) containing 150mM NaCl, is added to the microwell, and incubated for 30 to 90 minutes, most preferably for 60 minutes, at 35 to 45°C, most preferably at 40°C. After removal of the residual reaction mixture, a buffer solution of 100mM Tris-HCl(pH 7.5) containing 150mM NaCl/0.1% Tween-20 is added, incubated for 5 to 15 minutes, most preferably for 10 minutes, at 50 to 70°C, most preferably at 60°C, and then washed.

Step 6: Detection of enzyme reaction

The substrate for streptavidin-linked degradation enzyme was added to the microwell, and color or absorbance changes by enzyme reaction are detected: Synthetic peptides which show color or absorbance changes are desirable as substrates in degradation by the enzyme-substrate reaction. For example, in case of using streptavidin-alkaline phosphatase as a degradation enzyme, 100 $\mu$ l of pNPP(p-nitrophenyl phosphate) is added to the microwell, and

incubated for 60 to 120 minutes, most preferably for 90 minutes, at room temperature. After the reaction is stopped by addition of 1M NaOH, absorbance is measured at 405nm. Although the conventional spectrophotometer can be used to measure the absorbance, ELISA reader is a more desirable instrument to measure the absorbance of enzyme-substrate reaction mixture in microwells.

Also, the present invention provides a kit comprising the following components to implement the method described above: microwell whose inside has amine group, EDC solution and 1-methylimidazole solution, pH 7.0 for affixing a probe, 0.4M NaOH/0.25% Tween-20 solution for removing unaffixed probe, a solution containing dH<sub>2</sub>O, 20xSSPE/0.0167% Triton X-100 and salmon sperm DNA(10mg/ml) for blocking free amine groups on microwell surface, a solution of 0.5xSSC/0.1% Tween-20 for removing unhybridized biotinylated sample DNA fragments, a streptavidin-linked degradation enzyme to be bound to biotin, 100mM Tris-HCl(pH 7.5) solution containing 150mM NaCl for binding of streptavidin to biotin, 100mM Tris-HCl(pH 7.5) solution containing 150mM NaCl/0.1% Tween-20 for removing unbound streptavidin, and a substrate for the streptavidin-linked degradation enzyme.

In accordance with the present invention, mutated and non-mutated DNA samples can be differentiated by measuring biotin density bound to the microwell. That is, a degradation enzyme is bound to biotin, and activity of the bound enzyme can be assayed by addition of a substrate reacting with the degradation enzyme. In this way, the presence of mutation in the sample DNA can be detected and, furthermore, the type of the mutation can be identified. Therefore, in any experiments to detect DNA mutations, the results can be obtained in a more economical, simpler and safer way than any other conventional method as long as the portion of DNA to be identified can be amplified and a probe comprising the normal sequence corresponding to the

DNA to be identified can be prepared.

The method for identifying DNA mutation using microwells of the present invention provides the following advantages over conventional methods:

1. Since the same results can be obtained by using smaller amount of oligonucleotides than conventional methods, the invented method is more economical. Similar results in terms of absorbance can be obtained with 100ng of probe/well by employing the method of the invention while prior art method requires 600ng/well (see: Mol. Cell. Probes, 12:407-416, 1998).

2. In the prior art, microwells pretreated for binding oligonucleotides later were provided. Instead, oligonucleotide-affixed microwells are provided in the present invention, which in turn reduces the costs for oligonucleotide synthesis and microwell preparation as well.

3. When mutation is detected by using a conventional microwell having amine group to which oligonucleotides are to be bound, high absorbance of negative control is a major problem. By using microwells of present invention, the absorbance of negative control can be reduced remarkably.

4. Conventional methods for detecting DNA mutation in which sample DNA is affixed to microwell have problems such as secondary structures caused by length of sample DNA, weak binding affinity and complementary binding between sample nucleotide strands. These problems are solved in the invention by preaffixing DNA probe to the microwell.

5. The prior art uses membranes or gels whose handling is very cumbersome, and requires many complicated work accompanying the difficulties in handling large number of samples, while the invented method guarantees simplicity by performing entire steps in one well.

6. The prior art has many variations such as different ways of collecting samples and conducting experiments, which is an obstacle to performing experiments in a reproducible manner. The kit of the invention not

only provides the consistency in experimental condition, but also can be stored for a long period of time, which enables detection of large number of samples at the same time. Especially, since experimental errors may be avoided by using instruments, experimental data or type of samples can be analyzed statistically.

7. Results can be identified visually. That is, color changes resulting from enzymatic reaction can be detected with naked eyes, therefore, due to the obviousness of the result, the researcher can have confidence in the results.

The present invention is further illustrated in the following examples, which should not be taken to limit the scope of the invention.

Example 1: Identification of DNA mutation using microwells

The method for identifying DNA mutation of the invention involves procedures to detect the presence of mutation in patient's DNA by affixing a probe comprising the normal sequence corresponding to the DNA to be identified to the microwell, and then by assessing stability of the hybrid between a DNA sample and a complementary oligonucleotide probe immobilized on the microwell. As a representative example, the present inventors employed a direct sequenced region which is known to be uniquely found in genome of a Mycobacterium tuberculosis, BCG(Calmette-Guerin bacillus), and assessed the stability of duplexes of a sample DNA of a patient and various probes which include a probe of the normal nucleotide sequence of direct sequenced region, probes containing different types of mutations in the direct sequenced region, and a probe which is not related to the direct sequence as a negative control.

Example 1-1: The use of a probe comprising normal



## nucleotide sequence

First, primer a comprising a biotin-bound nucleotide sequence of 5'-GGTTTTGGGTCTGACGAC-3' (SEQ ID: 1) and primer b of 5'-CCGACAGGGGACGGAAAC-3' (SEQ ID: 2) were synthesized by the conventional method. And then, PCR was performed in a PCR mixture containing DNA (comprising direct sequence of BCG) to a final concentration of 200 ng/ $\mu$ l, 0.5  $\mu$ l of primer a (100 pmol/ $\mu$ l), 0.5  $\mu$ l of primer b (100 pmol/ $\mu$ l), 0.4  $\mu$ l of dNTP (25 mM), 10xTaq buffer, 3  $\mu$ l of MgCl<sub>2</sub> (25 mM), 0.2  $\mu$ l of Taq (5 unit/ $\mu$ l, Promega, U.S.A.) and 40.4  $\mu$ l of dH<sub>2</sub>O, with 30 cycles of denaturation (for 1 min. at 94°C), annealing (for 1 min. 30 sec. at 55°C) and extension (for 1 min. 30 sec. at 72°C).

Subsequently, probe #1 comprising a normal nucleotide sequence of 5'-TTGACCTCGCCAGGAGAGAAGATCA-3' (SEQ ID: 3) and probe #2 comprising a normal nucleotide sequence of 5'-TCCGTACGCTCGAAACGCTTCCAAC-3') was synthesized. 10 pmol aliquots of each probe were heated for 10 minutes at 94°C, cooled down for 10 minutes in ice water, condensed by centrifugation. And then, a solution of EDC and 1-methylimidazole pH 7.0 was added to the each aliquot of the probe to a final concentration of 10 mM. 100  $\mu$ l of each probe mixture thus prepared was introduced into microwells (Nunc, Denmark) on ice, incubated for 7 hours at 50°C. After removing the residual probe mixture, a solution containing 138  $\mu$ l of dH<sub>2</sub>O, 20xSSPE/0.0167% Triton X-100, and 2  $\mu$ l of salmon sperm DNA (10 mg/ml) was added to the microwells, and incubated for 20 minutes at 50°C for blocking free amine group on the microwell surface.

After removing the blocking solution, a sample mixture containing 68  $\mu$ l of dH<sub>2</sub>O, 30  $\mu$ l of 20xSSPE/0.0167% Triton X-100, 1  $\mu$ l of salmon sperm DNA (10 mg/ml) and 1  $\mu$ l of PCR amplified sample DNA prepared above was added to each microwell, and incubated for about 10 hours at 60°C. After removing the mixture, each microwell was washed 3 times with 200  $\mu$ l of 0.5x SSC, 0.1% Tween-20, and the same

solution was added to incubate for 15 minutes at 60°C. After washing 3 times with the same solution, 100  $\mu$ l of streptavidin-alkaline phosphatase prepared by 3000-fold dilution with a buffer solution of 100mM Tris-HCl (pH 7.5) containing 150mM NaCl was added to the microwell, and incubated for 1 hour at 40°C.

Subsequently, the microwells were washed 3 times with a buffer solution of 100mM Tris-HCl (pH 7.5) containing 150mM NaCl/0.1% Tween-20, and subjected to 3 times of incubation for 5 minutes at 60°C and washing with the same solution. 100  $\mu$ l of pNPP (N7653, Sigma, U.S.A) was added to each well, incubated for 90 minutes, and then the absorbance was measured at 405nm (see: Figure 1).

Example 1-2: The use of a probe with a substituted nucleotide

To identify a substitution mutation, probe #11 of 5'-TTGACCTCGCCAGAAGAGAAGATCA-3' (SEQ ID: 5) was synthesized by substituting the 14th nucleotide of probe #1, G with A, and probe #21 of 5'-TCCGTACGCTCGAGACGCTTCCAAC-3' (SEQ ID: 6) was synthesized by substituting the 14th nucleotide of probe #2, A with G. Then, identification of DNA mutation was performed in an analogous manner as in Example 1-1, except for employing the use of probes #11 and #21 instead of probes #1 and #2 (see: Figure 1).

Example 1-3: The use of a probe with an inserted nucleotide

To identify an insertion mutation, probe #12 of 5'-TTGACCTCGCCAGTGAGAGAAGATCA-3' (SEQ ID: 7) was synthesized by inserting T between 13th and 14th nucleotide of probe #1. Then, identification of DNA mutation was performed in an analogous manner as in Example 1-1, except for employing the use of probe #12 instead of probes #1 and #2 (see: Figure 1).

Example 1-4: The use of a probe with a deleted nucleotide

To identify a deletion mutation, probe #13 of 5'-TTGACCTCGCCAGAGAGAAGATCA-3'(SEQ ID: 8) was synthesized by deleting 14th nucleotide, G of probe #1. Then, identification of DNA mutation was performed in an analogous manner as in Example 1-1, except for employing the use of probe #13 instead of probes #1 and #2(see: Figure 1).

Example 1-5: The use of a negative control probe

For a negative control, probe #C of 5'-GGAGCTTTCGGCTTCTATCAGGTA-3'(SEQ ID: 9) comprising a nucleotide sequence which is found uniquely in a Mycobacterium tuberculosis, H37Rv, was synthesized. Then, identification of DNA mutation was performed in an analogous manner as in Example 1-1, except for employing the use of probe #C(see: Figure 1).

Figure 1 shows a graph, based on a direct sequenced region which is known to be uniquely found in the genome of Mycobacterium tuberculosis, BCG, demonstrating the identification of DNA mutation by assessing the stability of the duplex of a sample DNA from a patient and various probes which include a probe comprising a normal nucleotide sequence of direct sequenced region, probes containing different types of mutations in the direct sequenced region, and a probe which is not related to the direct sequence as a negative control. In Figure 1, No DNA represents a control without probe; No.1, a negative control, probe #C; No.2, probe #1 of normal sequence; No.3, probe #11 of substitution mutant; No.4, probe #13 of deletion mutant; No.5, probe #12 of insertion mutant; No.6, probe #2 of normal sequence; and, No.7, probe #21 of substitution mutant, respectively.

As shown in Figure 1, since the OD value from the

hybridization of the sample DNA with the probe of normal sequence showed the highest value, the sample DNA from a patient turned out to comprise the normal sequence. On the other hand, although the hybridization of a sample DNA with probes of mutated sequences made differences in OD values for each mutated probe more or less, the values were significantly lower than that for a probe of normal sequence, thus assuring that the presence of mutation can be clearly identified by the method of the invention.

The application of the invention make it possible to identify the position and the type of mutation by employing probes comprising each mutated sequence with one or more nucleotide changes.

As clearly illustrated and demonstrated above, the present invention can be applied to identify not only the presence of one or more mutations but also the types of mutations such as substitution, deletion and insertion in a more economical, simpler and safer way than any other conventional method.

WHAT IS CLAIMED IS:

1. A method for identifying DNA mutation using microwells which comprises the steps of:

5 (i) preparing amplified biotinylated DNA fragments of a portion of nucleotide sequence to be identified by PCR using a biotin-bound primer;

(ii) preparing a probe comprising normal sequence corresponding to the DNA sequence to be identified;

10 (iii) affixing the probe prepared in Step(ii) to the amine group of microwell;

(iv) adding biotinylated DNA fragments prepared in Step(i) to the probe-affixed microwell;

15 (v) adding a streptavidin-linked degradation enzyme to the microwell in order to bind the degradation enzyme to biotin moiety of the probe-captured sample DNA fragment; and,

20 (vi) adding a substrate to be reacted with the degradation enzyme and detecting the color or absorbance change caused by degradation of the substrate.

25 2. The method for identifying DNA mutation of claim 1, wherein the probe is a nucleotide sequence consisting of more than 10 nucleotides and containing a phosphate moiety at 5' end.

30 3. The method for identifying DNA mutation of claim 1, wherein Step(iii) comprises adding single-stranded probe to the microwell, adding catalysts in order to bind the phosphate moiety of the single-stranded probe to the amine group of microwell, and washing the microwell.

35 4. The method for identifying DNA mutation of claim 3, wherein the catalysts are ice-cold solutions of 10mM 1-methylimidazole, pH 7.0 and 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide(EDC), pH 7.0.

5. The method for identifying DNA mutation of claim 3, wherein the washing is performed by employing 0.4M NaOH/0.25% Tween-20 solution.

5           6. The method for identifying DNA mutation of claim 1, wherein Step(iv) comprises binding single-stranded DNA fragments obtained in Step(i) to the probe of microwell, removing the residual DNA fragments, and washing the microwell.

10           7. The method for identifying DNA mutation of claim 6, further comprising pretreatment of the microwell with a solution containing dH<sub>2</sub>O, 20xSSPE/0.0167% Triton X-100 and salmon sperm DNA(10mg/ml) at 50°C for 20 minutes before  
15           adding the single-stranded DNA fragments obtained in Step(i) to the microwell.

20           8. The method for identifying DNA mutation of claim 6, wherein binding the DNA fragments obtained in Step(i) to the probe occurs in a solution containing dH<sub>2</sub>O, 20xSSPE/0.0167% Triton X-100 and salmon sperm DNA(10mg/ml).

25           9. The method for identifying DNA mutation of claim 6, wherein the washing is performed by employing 0.5xSSC/0.1% Tween-20 solution.

30           10. The method for identifying DNA mutation of claim 1, wherein Step(v) comprises the first washing of the microwell, introducing streptavidin-linked degradation enzyme to the microwell for binding of the enzyme with biotin, removing the residual reaction mixture, and the second washing of the microwell.

35           11. The method for identifying DNA mutation of claim 10, wherein the first washing is performed by employing a buffer solution of 100mM Tris-HCl(pH 7.5) containing 150mM NaCl/0.1% Tween-20.

12. The method for identifying DNA mutation of claim 10, wherein the streptavidin-linked degradation enzyme is streptavidin-alkaline phosphatase dissolved in a buffer solution of 100mM Tris-HCl(pH 7.5) containing 150mM NaCl.

13. The method for identifying DNA mutation of claim 10, wherein the second washing comprises treatment of the microwell with a buffer solution of 100mM Tris-HCl(pH 7.5) containing 150mM NaCl/0.1% Tween-20 at 60°C for 10 minutes.

14. The method for identifying DNA mutation of claim 1, wherein the substrate to be reacted with streptavidin-linked degradation enzyme is a synthetic peptide showing color or absorbance change during the degradation.

15. The method for identifying DNA mutation of claim 14, wherein the substrate is pNPP(p-nitrophenyl phosphate) provided that the streptavidin-linked degradation enzyme of streptavidin-alkaline phosphatase is employed.

16. The method for identifying DNA mutation of claim 1, wherein the color change is detected with naked eyes.

17. The method for identifying DNA mutation of claim 1, wherein the absorbance is measured by employing an ELISA reader.

18. A kit for identifying DNA mutation which comprises:

(i) a microwell whose inside has amine group;  
(ii) 10mM 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide(EDC), pH 7.0 and 10mM 1-methylimidazole, pH 7.0;

(iii) 0.4M NaOH/0.25% Tween-20 solution;  
(iv) a solution containing dH<sub>2</sub>O, 20xSSPE/0.0167% Triton X-100 and salmon sperm DNA(10mg/ml);

- (v) 0.5xSSC/0.1% Tween-20 solution;
- (vi) streptavidin-alkaline phosphatase;
- (vii) 100mM Tris-HCl(pH 7.5) solution containing 150mM NaCl;
- 5 (viii) 100mM Tris-HCl(pH 7.5) solution containing 150mM NaCl/0.1% Tween-20; and,
- (ix) pNPP(p-nitrophenyl phosphate).



,09979545

1/1

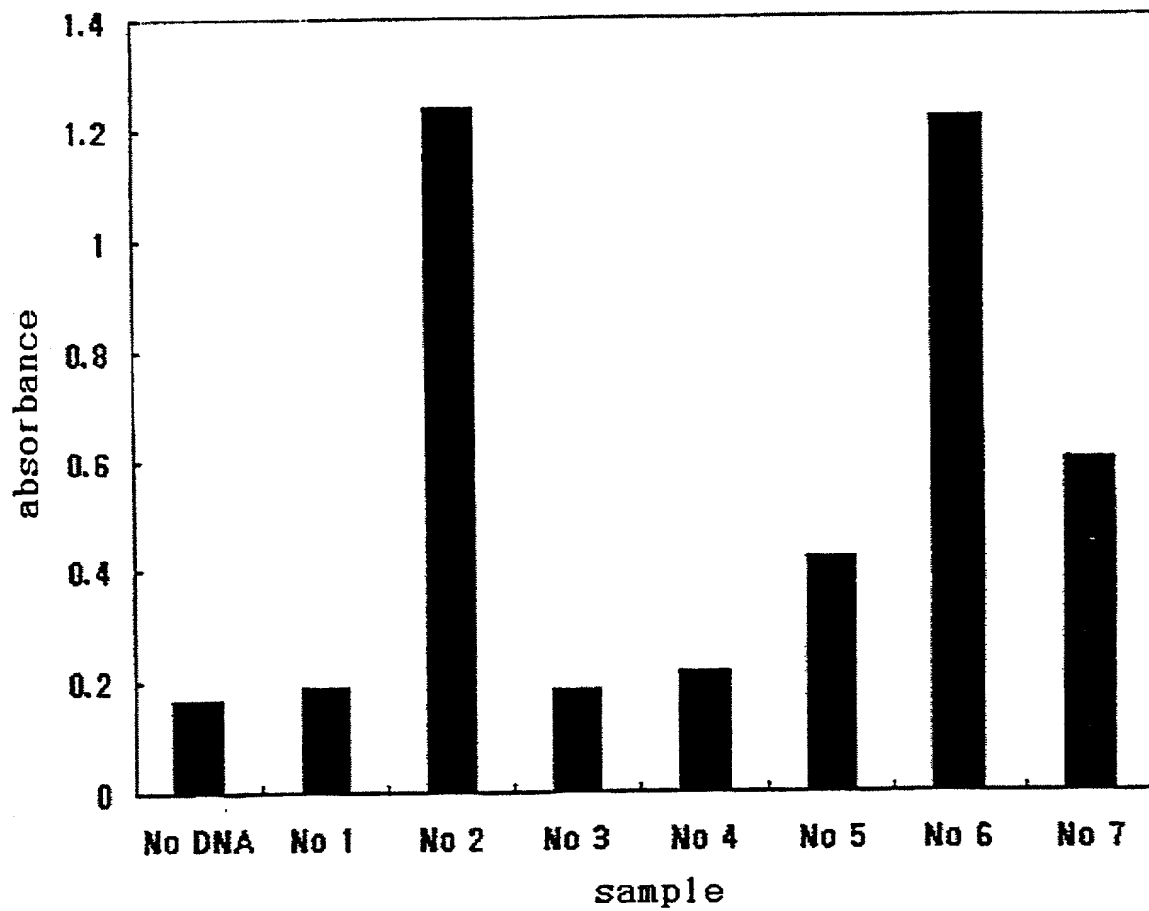


Fig. 1

**DECLARATION AND POWER OF ATTORNEY - USA PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name;

I believe I am the original, first and sole inventor (in only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

**"A Method for Identifying DNA Mutation Using Microwell and Kit Therefor"**

the specification of which is attached hereto.

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above;

I acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulation, § 1.56;

I hereby claim foreign priority benefits under Title 35, United States Code, § 119 of any foreign application(s) for patent, design or inventor's certificate or any PCT international application(s) listed below and have also identified below any foreign application(s) for patent, design or inventor's certificate or any PCT international application(s) designating at least one country other than the United States of America filed for the same subject matter having a filing date before that of the application(s) of which priority is claimed:

**PRIOR FOREIGN APPLICATION(S)**

COUNTRY (OR INDICATE IF PCT)	APPLICATION NUMBER	DATE OF FILING (day/month/year)	PRIORITY CLAIMED UNDER 37 U.S.C. § 119
Republic of Korea	10-1999-0019121	26/May/1999	[ X ] YES      NO [   ]
PCT	PCT/KR00/00535	25/May/2000	[   ] YES      NO [ X ]
			[   ] YES      NO [   ]
			[   ] YES      NO [   ]
			[   ] YES      NO [   ]

I hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s) listed below, and insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code § 112, I acknowledge the duty to disclose to the U.S. Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, § 1.56, which became available between the filing date of the prior application and the national or PCT international filing date of this application:

Prior U.S.A. Application(s)

Application No.:

Filing Date:

Status:

**POWER OF ATTORNEY:** I hereby appoint the registrants of Knobbe, Martens, Olson & Bear, LLP, 620 Newport Center Drive, Sixteenth Floor, Newport Beach, California 92660, Telephone (949) 760-0404, **Customer No. 20,995.**

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful, false statements may jeopardize the validity of the application or any patent issued thereon.

Full name of sole or first inventor: 1-00 HWANG, Seung-Yong

Inventor's signature

HWANG

8<sup>th</sup> Day

November

Month 2001 Year

Residence(city and country): Ansan, Republic of Korea

Citizenship:

Republic of Korea

KRX

Post Office Address: at

Sunkyung Apartment 103-603, Sa 2-dong, Ansan, Kyunggi-do 425-172,  
Republic of Korea

Full name of sole or second inventor: 2-00 JUNG, Jin-Wook

Inventor's signature

JUNG

8<sup>th</sup> Day

November

Month 2001 Year

Residence(city and country): Seoul, Republic of Korea

Citizenship:

Republic of Korea

KRX

Post Office Address:

Samho Apartment 1-403, Bangbaebon-dong, Seocho-gu, Seoul 137-069,  
Republic of Korea

Full name of sole or third inventor: <sup>3-00</sup> KIM, Cheol-Min

Inventor's signature 김철민 8<sup>th</sup> Day November Month 2001 Year

Residence(city and country): Pusan, Republic of Korea

Citizenship: Republic of Korea KRX

Post Office Address: Samik Apartment 211-811, 148 Namchon 2-dong, Sooyoung-gu, Pusan  
613-012, Republic of Korea

Send Correspondence To:  
KNOBBE, MARTENS, OLSON & BEAR  
620 Newport Center Drive  
Sixteenth Floor  
Newport Floor, CA 92660-8016

Direct Telephone Calls To:

(949)760-0404

Inventor or Patentee: HWANG, Seung-Yong, et al.

Case No.:

Page 1

Applicant or Patent No.:

Filed or Issued:

Title: "A METHOD FOR IDENTIFYING DNA MUTATION USING MICROWELL AND KIT THEREFOR"

**VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS**

1. I, the undersigned, do hereby declare that:

- a. ☒ I am an independent inventor as defined in 37 CFR 1.9(c) for purposes of paying reduced fees to the Patent and Trademark Office with regard to the invention described in the patent or application identified above; OR
- b. ☐ While I am not an inventor, I declare that rights under contract or law have been conveyed to and remain with me with regard to the invention described in the patent or application identified above. I would qualify as an independent inventor as defined in 37 CFR 1.9(c) for purposes of paying fees to the United States Patent and Trademark Office if I had made the invention; OR
- c. ☐ I am the owner of the small business concern identified below  
OR  
☐ I am an official of the small business concern empowered to act on behalf of the concern identified below:

NAME OF SMALL BUSINESS:

ADDRESS OF SMALL BUSINESS:

If either of the boxes in item (c) is checked, I further declare that the above-identified small business concern qualifies as a small business concern as defined in 13 CFR 121.12, and reproduced in 37 CFR 1.9(d), for purposes of paying reduced fees to the United States Patent and Trademark Office, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third party or parties controls or has the power to control both. I further declare that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention described in the patent or application identified above; or

- d. ☐ I am an official empowered to act on behalf of the nonprofit organization identified below:

NAME OF NONPROFIT ORGANIZATION:

ADDRESS OF NONPROFIT ORGANIZATION:

Inventor or Patentee: HWANG, Seung-Yong, et al. Case No.: Page 2  
 Applicant or Patent No.:  
 Filed or Issued:  
 Title: "A METHOD FOR IDENTIFYING DNA MUTATION USING MICROWELL AND KIT THEREFOR"

TYPE OF NONPROFIT ORGANIZATION:

- ☐ university or other institution of higher education  
☐ tax exempt under Internal Revenue Service Code(26 USC 501(a) and 501(c)(3))  
☐ nonprofit scientific or educational under statute of state of the United States of America  
     (name of state: )  
     (citation of statute: )  
☐ would qualify as tax exempt under Internal Revenue Service Code(26 USC 501(a) and 501(c)(3)) if located in the United States of America  
☐ would qualify as nonprofit scientific or educational under statute of state of the United States of America if located in the United States of America  
     (name of state: )  
     (citation of statute: )

If Box(d) is checked, I further declare that the nonprofit organization identified above qualifies as a nonprofit organization as defined in 37 CFR 1.9(e) for purposes of paying reduced fees to the United States Patent and Trademark Office regarding the invention described in the patent or application identified above.

2. The individual, concern or organization identified above has not assigned, granted, conveyed or licensed, and is under no obligation under contract or law to assign, grant, convey or license, any rights in the invention to any person who would not qualify as an independent inventor under 37 CFR 1.9(c) if that person had made the invention, or to any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e).
3. If the rights held by above-identified individual, concern or organization are not exclusive, each individual, concern or organization having rights in the invention are identified below. Each such individual, concern or organization must file separate verified statements averring to their status as small entities.

**\*Note: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27).**

FULL NAME:

ADDRESS:

☐ INDIVIDUAL ☐ SMALL BUSINESS CONCERN ☐ NONPROFIT ORGANIZATION

FULL NAME:

ADDRESS:

☐ INDIVIDUAL ☐ SMALL BUSINESS CONCERN ☐ NONPROFIT ORGANIZATION

Inventor or Patentee: HWANG, Seung-Yong, et al.

Case No.:

Page 3

Applicant or Patent No.:

Filed or Issued:

Title: "A METHOD FOR IDENTIFYING DNA MUTATION USING MICROWELL AND KIT THEREFOR"

4. I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small-entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 CFR 1.28(b)).

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

NAME OF PERSON SIGNING: HWANG, Seung-Yong

TITLE OF PERSON (if not an owner or individual):

ADDRESS OF PERSON SIGNING: Sunkyung Apartment 103-603, Sa 2-dong, Ansan, Kyunggi-do  
425-172, Republic of Korea

NAME OF PERSON SIGNING: JUNG, Jin-Wook

TITLE OF PERSON (if not an owner or individual):

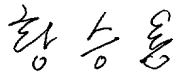
ADDRESS OF PERSON SIGNING: Samho Apartment 1-403, Bangbaebon-dong, Seocho-gu,  
Seoul 137-069, Republic of Korea

NAME OF PERSON SIGNING: : KIM, Cheol-Min

TITLE OF PERSON (if not an owner or individual):

ADDRESS OF PERSON SIGNING: Samik Apartment 211-811, 148 Namchon 2-dong, Sooyoung-gu,  
Pusan 613-012, Republic of Korea

SIGNATURE:



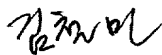
DATE: Nov. 8, 2001

SIGNATURE:



DATE: Nov. 8, 2001

SIGNATURE:



DATE: Nov. 8, 2001

## Sequence Listing

<110> HWANG, Seung-Yong

<120> A Method for Identifying DNA Mutation Using Microwells and Kit therefor

<160> 9

<170> KOPATIN 1.5

<210> 1

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 1

ggttttgggt ctgacgac

18

<210> 2

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 2

ccgacagggg acggaac

18

<210> 3



<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR product

<400> 3  
ttgacctgc caggagagaa gatca

25

<210> 4  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR product

<400> 4  
tccgtacgct cgaacgctt ccaac

25

<210> 5  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR product

<400> 5  
ttgacctgc cagaagagaa gatca

25

<210> 6  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR product

<400> 6  
tccgtacgct cgagacgctt ccaac

25

<210> 7  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR product

<400> 7  
ttgacctcgc cagtgagaga agatca

26

<210> 8  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR product

<400> 8  
ttgacctcgc cagagagaag atca

24

<210> 9  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR product

<400> 9

ggagcttcc ggcttctatc aggta

25